50334386

FILE 'CAPLUS' ENTERED AT 15:46:29 ON 07 OCT 2004
L1 57 (PROTEIN? OR PEPTIDE? OR POLYPEPTID?) (S) MALDI (S) STANDARD?
L2 6 L1 AND (DERIVAT? OR ISOFORM?)
L3 24 (PROTEIN? OR PEPTIDE? OR POLYPEPTID?) (S) CRYSTAL? (S) MALDI
L4 0 MALDI (S)(("CO-CRYSTALLIZATION" OR "CO-CRYSTALLIZING" OR "CO-CRYSTALS") (6A) (PROTEIN? OR PEPTIDE? OR POLYPEPTID?))
L5 0 MALDI (S)(("CO-CRYSTALLIZATION" OR "CO-CRYSTALLIZING" OR "CO-CRYSTALS") (S) (PROTEIN? OR PEPTIDE? OR POLYPEPTID?))
L6 2 MALDI AND ("CO-CRYSTALLIZATION" OR "CO-CRYSTALLIZING" OR "CO-CRYSTALS") AND (PROTEIN? OR PEPTIDE? OR POLYPEPTID?)

L2 ANSWER 1 OF 6 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2004:600936 CAPLUS
DOCUMENT NUMBER: 141:239079
TITLE: MALDI-MS analysis of peptides modified with photolabile arylazido groups
AUTHOR(S): Low, William; Kang, James; DiGruccio, Michael; Kirby, Dean; Perrin, Marilyn; Fischer, Wolfgang H.
CORPORATE SOURCE: The Clayton Foundation Laboratories for Peptide Biology, The Salk Institute, La Jolla, CA, USA
SOURCE: Journal of the American Society for Mass Spectrometry (2004), 15(8), 1156-1160
CODEN: JAMSEF; ISSN: 1044-0305
PUBLISHER: Elsevier Inc.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The ability of MALDI-MS to analyze photolabile arylazido peptide derivs. was investigated. Peptides containing UV-labile p-azidobenzoyl groups were subjected to MALDI-MS anal. in a variety of matrixes. As standard MALDI-MS employs a UV laser (337 nm), we investigated conditions that would allow detection of the intact mol. ions for these light-sensitive peptides. When using <SYM97>-cyano-4-hydroxycinnamic acid (ACHC) or 2,5 dihydroxybenzoic acid (DHB) as the matrix, photoinduced degradation products were prevalent. In contrast, when employing the matrix sinapinic acid, the intact mol. ion corresponding with the azido peptide was the predominant signal. The protection of photolabile azido derivs. correlates with the UV absorbance properties of the matrix employed, i.e., sinapinic acid, which exhibits a strong absorbance near 337 nm, most efficiently protects the azido derivative from photodegrdn.
REFERENCE COUNT: 11

L2 ANSWER 2 OF 6 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2004:375861 CAPLUS
TITLE: MALDI-MS analysis of peptides modified with photolabile arylazido groups
AUTHOR(S): Low, William; Kang, James; DiGruccio, Micheal; Kirby, Dean; Perrin, Marilyn; Fischer, Wolfgang H.
CORPORATE SOURCE: The Salk Institute, La Jolla, CA, 92037, USA

SOURCE: Methods in Proteome and Protein Analysis (2004), 261-268. Editor(s): Kamp, Roza Maria; Calvete, Juan J.; Choli-Papadopoulou, Theodora. Springer-Verlag: Berlin, Germany.
CODEN: 69FJLW; ISBN: 3-540-20222-6
DOCUMENT TYPE: Conference
LANGUAGE: English
AB The ability of MALDI-MS to analyze photolabile arylazido peptide derivs. was investigated. Peptides containing UV-labile p-azidobenzoyl groups were subjected to MALDI-MS anal. in a variety of matrixes. As a standard MALDI-MS employs a UV laser (337 nm), we investigated conditions that would allow detection of the intact mol. ions for these modified peptides. When using <SYM97>-cyano-4-hydroxycinnamic acid (ACHC) or 2,5 dihydroxybenzoic acid (DHB) as the matrix, photoinduced degradation products were prevalent. In contrast, when employing the matrix sinapinic acid, the intact mol. ion corresponding with the azido peptide was the predominant signal. The protection of photolabile azido derivs. correlates with the UV absorbance properties of the matrix employed, i.e. sinapinic acid which exhibits a strong absorbance near 337 nm most efficiently protects the azido derivative from photodegrdn. REFER. COUNT: 9

L2 ANSWER 3 OF 6 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2004:75321 CAPLUS
DOCUMENT NUMBER: 140:356032
TITLE: BSE control: Detection of gelatine-derived peptides in animal feed by mass spectrometry
AUTHOR(S): Fernandez Ocana, Mireia; Neubert, Hendrik; Przyborowska, Anna; Parker, Richard; Bramley, Peter; Halket, John; Patel, Raj
CORPORATE SOURCE: Centre for Chemical and Bioanalytical Sciences, Royal Holloway University of London, Egham, TW20 0EX, UK
SOURCE: Analyst (Cambridge, United Kingdom) (2004), 129(2), 111-115
CODEN: ANALAO; ISSN: 0003-2654
PUBLISHER: Royal Society of Chemistry
DOCUMENT TYPE: Journal
LANGUAGE: English
AB This has led to a ban of feeding animals with "processed animal protein" (PAP). The authors report a novel approach for the mass spectrometric detection of processed animal protein (PAP) contamination in animal feedstuffs by detecting gelatine, a derivative of the major animal protein collagen. A method was developed to hydrolyze gelatine stds. with hydrochloric acid, followed by detection of the derived hydrolytic peptides at m/z 828, 915, 957 and 1044 by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) and liquid chromatog. electrospray ionization mass spectrometry (LC-ESI-MS-MS). The marker peptides can be detected at concns. of 100 ng ml-1 gelatine in water with MALDI. The procedure was adapted to obtain a suitable peptide map of gelatine extracted from spiked feed. The ratio of signal area of the gelatine-derived peptide at m/z 1044 to the internal standard at m/z 556 is shown to relate to the total amount of gelatine present in the sample.
REFERENCE COUNT: 22

L2 ANSWER 4 OF 6 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2003:876862 CAPLUS
DOCUMENT NUMBER: 140:55853
TITLE: "Stable-isotope dimethyl labeling for quantitative proteomics"
AUTHOR(S): *Hsu, Jue-Liang; Huang, Sheng-Yu; Chow, Nan-Haw; Chen, Shu-Hui*
CORPORATE SOURCE: Department of Chemistry, National Cheng Kung University, Tainan, 701, Taiwan
SOURCE: **Analytical Chemistry (2003), 75(24), 6843-6852**
CODEN: ANCHAM; ISSN: 0003-2700
PUBLISHER: American Chemical Society
DOCUMENT TYPE: Journal
LANGUAGE: English
AB In this paper, we report a novel, stable-isotope labeling strategy for quant. proteomics that uses a simple reagent, formaldehyde, to globally label the N-terminus and <SYM101>-amino group of Lys through reductive amination. This labeling strategy produces peaks differing by 28 mass units for each derivatized site relative to its nonderivatized counterpart and 4 mass units for each derivatized isotopic pair. This labeling reaction is fast (less than 5 min) and complete without any detectable byproducts based on the anal. of MALDI and LC/ESI-MS/MS spectra of both derivatized and nonderivatized peptide stds. and tryptic peptides of Hb mols. The intensity of the a1 and yn-1 ions produced, which were not detectable from most of the nonderivatized fragments, was substantially enhanced upon labeling. We further tested the method based on the anal. of an isotopic pair of peptide stds. and a pair of defined protein mixts. with known H/D ratios. Using LC/MS for quantification and LC/MS/MS for peptide sequencing, the results show a negligible isotopic effect, a good mass resolution between the isotopic pair, and a good correlation between the exptl. and theor. data (errors 0-4%). The relative standard deviation of H/D values calculated from peptides deduced from the same protein are less than 13%. The applicability of the method for quant. protein profiling was also explored by analyzing changes in nuclear protein abundance in an immortalized E7 cell with and without arsenic treatment. REFERENCE COUNT: 25

L2 ANSWER 5 OF 6 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2003:767340 CAPLUS
DOCUMENT NUMBER: 139:347687
TITLE: "High sequence coverage of proteins isolated from liquid separations of breast cancer cells using capillary electrophoresis-time-of-flight MS and MALDI-TOF MS mapping"
AUTHOR: *Zhu, Kan; Kim, Jeongkwon; Yoo, Chul; Miller, Fred R.; Lubman, David M.*
CORPORATE SOURCE: Department of Chemistry, The University of Michigan, Ann Arbor, MI, 48109-1055, USA
SOURCE: **Analytical Chemistry (2003), 75(22), 6209-6217**
CODEN: ANCHAM; ISSN: 0003-2700
PUBLISHER: American Chemical Society
DOCUMENT TYPE: Journal
LANGUAGE: English

AB A method has been developed for high sequence coverage anal. of proteins isolated from breast cancer cell lines. Intact proteins are isolated using multidimensional liquid-phase sepns. that permit the collection of individual protein fractions. Protein digests are then analyzed by both matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) peptide mass fingerprinting and by capillary electrophoresis-electrospray ionization (CE-ESI)-TOF MS peptide mapping. These methods can be readily interfaced to the relatively clean proteins resulting from liquid-phase fractionation of cell lysates with little sample preparation Using combined sequence information provided by both mapping methods, 100% sequence coverage is often obtained for smaller proteins, while for larger proteins up to 75 kDa, over 90% coverage can be obtained. Furthermore, an accurate intact protein MW value (within 150 ppm) can be obtained from ESI-TOF MS. The intact MW together with high coverage sequence information provides accurate identification. More notably the high sequence coverage of CE-ESI-TOF MS together with the MS/MS information provided by the ion trap/reTOF MS elucidates posttranslational modifications, sequence changes, truncations, and isoforms that may otherwise go undetected when standard MALDI-MS peptide fingerprinting is used. This capability is critical in the anal. of human cancer cells where large nos. of expressed proteins are modified, and these modifications may play an important role in the cancer process. REFERENCE COUNT: 51

L2 ANSWER 6 OF 6 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2000:55650 CAPLUS
DOCUMENT NUMBER: 132:171649
TITLE: Fraction collection in micropreparative capillary zone electrophoresis and capillary isoelectric focusing
AUTHOR(S): Minarik, Marek; Foret, Frantisek; Karger, Barry L.
CORPORATE SOURCE: Barnett Institute and Department of Chemistry, Northeastern University, Boston, MA, 02115, USA
SOURCE: Electrophoresis (2000), 21(1), 247-254
CODEN: ELCTDN; ISSN: 0173-0835
PUBLISHER: Wiley-VCH Verlag GmbH
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A new fraction collection system for capillary zone electrophoresis (CZE) and capillary isoelec. focusing (CIEF) is described. Exact timing of the collector steps was based on determining the velocity of each individual zone measured between 2 detection points close to the end of the capillary. Determination of the zone velocity shortly before collection overcame the need for constant analyte velocity throughout the column. Consequently, sample stacking in CZE with large injection vols. as well as zone focusing in CIEF could be used with high collection accuracy. Capillaries of 200 <SYM109>m inner diameter (ID) were employed in CZE and 100 <SYM109>m ID in CIEF for the micropreparative mode. A sheath flow fraction collector was used to maintain permanent elec. current during the collection. The bulk liquid flow due to siphoning, as well as the backflow arising from the sheath flow droplet pressure, were suppressed by closing the separation system at the inlet with a semipermeable membrane. In the CZE mode, the performance of the fraction collector is demonstrated by isolation of individual peaks

from a fluorescently derivatized oligosaccharide ladder. In the CIEF mode, collection of several proteins from a mixture of stds. is shown, followed by subsequent anal. of each protein fraction by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF-MS). REFERENCE COUNT: 50

L1 ANSWER 1 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN
TI MALDI-MS analysis of peptides modified with photolabile arylazido groups
L1 ANSWER 2 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN
TI Analysis of protein glycation products by matrix-assisted laser desorption ionization time-of-flight mass spectrometry
L1 ANSWER 3 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN
TI MALDI-MS analysis of peptides modified with photolabile arylazido groups
L1 ANSWER 4 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN
TI MALDI MS peptide mapping performance by in-gel digestion on a probe with prestructured sample supports
L1 ANSWER 5 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN
TI Nonredundant mass spectrometry: a strategy to integrate mass spectrometry acquisition and analysis
L1 ANSWER 6 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN
TI Tracking cell signaling protein expression and phosphorylation by innovative proteomic solutions
L1 ANSWER 7 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN
TI Direct determination of the peptide content in microspheres by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry
L1 ANSWER 8 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN
TI Acid-labile surfactant improves in-sodium dodecyl sulfate polyacrylamide gel protein digestion for matrix-assisted laser desorption/ionization mass spectrometric peptide mapping
L1 ANSWER 9 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN
TI BSE control: Detection of gelatine-derived peptides in animal feed by mass spectrometry
L1 ANSWER 10 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN
TI Combining Liquid Chromatography with MALDI Mass Spectrometry Using a Heated Droplet Interface
L1 ANSWER 11 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN
TI Integrated sample preparation and MALDI mass spectrometry on a microfluidic compact disk
L1 ANSWER 12 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN
TI Qualitative and quantitative proteomics by two-dimensional gel electrophoresis, peptide mass fingerprint and a chemically-coded affinity tag (CCAT)
L1 ANSWER 13 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN
TI Stable-isotope dimethyl labeling for quantitative proteomics
L1 ANSWER 14 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN
TI Single-step perfusion chromatography with a throughput potential for enhanced peptide detection by matrix-assisted laser desorption/ionization- mass spectrometry
L1 ANSWER 15 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN

TI Matched filtration with experimental noise determination for denoising, peak picking, and quantitation in LC-MS

L1 ANSWER 16 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN

TI Closely spaced external standard: A universal method of achieving 5 ppm mass accuracy over the entire MALDI plate in axial matrix-assisted laser desorption/ionization time-of-flight mass spectrometry

L1 ANSWER 17 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN

TI High sequence coverage of proteins isolated from liquid separations of breast cancer cells using capillary electrophoresis-time-of-flight MS and MALDI-TOF MS mapping

L1 ANSWER 18 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN

TI Analysis of relative isotopologue abundances for quantitative profiling of complex protein mixtures labelled with the acrylamide/D3-acrylamide alkylation tag system

L1 ANSWER 19 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN

TI Quantitative analysis of complex peptide reaction systems by mass spectrometry

L1 ANSWER 20 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN

TI Fast-response proteomics by accelerated in-gel digestion of proteins

L1 ANSWER 21 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN

TI Continuous sample deposition from reversed-phase liquid chromatography to tracks on a matrix-assisted laser desorption/ionization precoated target for the analysis of protein digests

L1 ANSWER 22 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN

TI A protein molecular weight map of ES2 clear cell ovarian carcinoma cells using a two-dimensional liquid separations/mass mapping technique

L1 ANSWER 23 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN

TI The use of DODT as a non-malodorous scavenger in Fmoc-based peptide synthesis

L1 ANSWER 24 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN

TI Acid effects on protein molecular weight determination

L1 ANSWER 25 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN

TI Relationship between MALDI-TOF Analysis of <SYM98>-CN f193-209 Concentration and Sensory Evaluation of Bitterness Intensity of Aged Cheddar Cheese

L1 ANSWER 26 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN

TI Quantification of protein-polymer interactions by matrix-assisted laser desorption/ ionization mass spectrometry

L1 ANSWER 27 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN

TI Quantitative MALDI-time of flight mass spectrometry of peptides and proteins

L1 ANSWER 28 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN

TI A 2-D liquid separations/mass mapping method for interlysate comparison of ovarian cancers

L1 ANSWER 29 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN

TI Off-line coupling of high-resolution capillary electrophoresis to MALDI-TOF and TOF/TOF MS

L1 ANSWER 30 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN

TI On-target fraction collection for the off-line coupling of capillary isoelectric focusing with matrix-assisted laser desorption/ionization mass spectrometry

L1 ANSWER 31 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN

TI Disposable polymeric high-density nanovial arrays for matrix assisted laser desorption/ionization-time of flight-mass spectrometry: I. Microstructure development and manufacturing

L1 ANSWER 32 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN

TI Simplified sample preparation method for protein identification by matrix-assisted laser desorption/ionization mass spectrometry: in-gel digestion on the probe surface

L1 ANSWER 33 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN

TI Simplified sample preparation method for protein identification by matrix-assisted laser desorption/ionization mass spectrometry: in-gel digestion on the probe surface

L1 ANSWER 34 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN

TI Evaluation of the efficiency of in-gel digestion of proteins by peptide isotopic labeling and MALDI mass spectrometry

L1 ANSWER 35 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN

TI On-membrane digestion of <SYM98>-casein for determination of phosphorylation sites by matrix-assisted laser desorption/ionization quadrupole/time-of-flight mass spectrometry

L1 ANSWER 36 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN

TI Single molecule detector for mass spectrometry with mass independent detection efficiency

L1 ANSWER 37 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN

TI A microsystem platform interfacing MALDI-TOF MS for high speed automated protein identification

L1 ANSWER 38 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN

TI Quantitation of peptides and proteins by matrix-assisted laser desorption/ionization mass spectrometry using 18O-labeled internal standards

L1 ANSWER 39 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN

TI Signature-peptide approach to detecting proteins in complex mixtures

L1 ANSWER 40 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN

TI Fraction collection in micropreparative capillary zone electrophoresis and capillary isoelectric focusing

L1 ANSWER 41 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN

TI Matrix-assisted laser desorption/ionization mass spectrometry, enzymatic digestion, and molecular modeling in the study of nonenzymatic glycation of IgG

L1 ANSWER 42 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN

TI Quantitative determination of the peptide retention of polymeric substrates using matrix-assisted laser desorption/ionization mass spectrometry

L1 ANSWER 43 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN

TI Integrated Microanalytical Technology Enabling Rapid and Automated Protein Identification

L1 ANSWER 44 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN

TI Direct TLC-MALDI Coupling Using a Hybrid Plate

L1 ANSWER 45 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN

TI MALDI- and ESI-mass spectrometric investigation of homo- and heterobifunctional crosslinking reagents for proteins

L1 ANSWER 46 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN

TI Approaches to the characterization of membrane channel proteins (porins) by UV MALDI-MS

L1 ANSWER 47 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN
TI Investigations of 2,5-DHB and succinic acid as matrixes for UV and IR MALDI. Part II: crystallographic and mass spectrometric analysis

L1 ANSWER 48 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN
TI Capillary LC with automated online microfraction collection onto MALDI/TOF MS targets

L1 ANSWER 49 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN
TI Rapid mass spectrometric identification of proteins from two-dimensional polyacrylamide gels after in gel proteolytic digestion

L1 ANSWER 50 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN
TI Selection of internal standards for quantitative analysis by matrix-assisted laser desorption-ionization (MALDI) time-of-flight mass spectrometry

L1 ANSWER 51 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN
TI Ultraviolet matrix assisted laser desorption ionization-mass spectrometry of electroblotted proteins

L1 ANSWER 52 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN
TI Mass Spectrometric Sequencing of Proteins from Silver-Stained Polyacrylamide Gels

L1 ANSWER 53 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN
TI Polyethylene Membrane as a Sample Support for Direct Matrix-Assisted Laser Desorption/Ionization Mass Spectrometric Analysis of High Mass Proteins

L1 ANSWER 54 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN
TI Matrix Dependence of Metastable Fragmentation of Glycoproteins in MALDI TOF Mass Spectrometry

L1 ANSWER 55 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN
TI Improved Resolution and Very High Sensitivity in MALDI TOF of Matrix Surfaces Made by Fast Evaporation

L1 ANSWER 56 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN
TI Quantitative analysis of peptides by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry

L1 ANSWER 57 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN
TI Direct determination of forskolin-bovine serum albumin conjugate by matrix-assisted laser desorption ionization mass spectrometry

=> d l1 ibib abs 2, 6, 12, 13, 14, 16, 18, 19, 22, 27, 28, 30, 36, 37, 38, 50

L1 ANSWER 2 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2004:571677 CAPLUS
TITLE: Analysis of protein glycation products by matrix-assisted laser desorption ionization time-of-flight mass spectrometry
AUTHOR(S): Kislinger, Thomas; Humeny, Andreas; Pischetsrieder, Monika
CORPORATE SOURCE: Institut fuer Pharmazie und Lebensmittelchemie, Emil-Fischer-Zentrum, Friedrich-Alexander Universitaet Erlangen-Nuernberg, Erlangen, 91052, Germany
SOURCE: Current Medicinal Chemistry (2004), 11(16), 2185-2193

CODEN: CMCHE7; ISSN: 0929-8673
PUBLISHER: Bentham Science Publishers Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The term protein glycation summarizes non-enzymic reactions between amino groups of proteins and sugars or sugar degradation products, leading to early glycation products (intact sugar attached) and advanced glycation end-products (AGEs). Protein glycation is involved in the progression of several diseases, such as diabetes, uremia, and atherosclerosis. However, qual. and quant. anal. of in vitro or in vivo glycated proteins is still a challenging task. The introduction of matrix-assisted laser desorption ionization time-of-flight technique (MALDI-TOF) changed mass spectrometry (MS) into a valuable tool for biomedical anal., because the soft ionization procedure allows the measurement of proteins up to 100 kDa. In the last few years, MALDI-TOF-MS was applied to the investigation of glycation processes: the analyses of plasma proteins from diabetic or uremic patients allowed a precise determination of the average number of sugar residues attached to serum albumin or Igs of each patient. Thus, a more individualized diagnosis of each patient was achieved by MALDI-TOF-MS than by other diagnostic tools. In a similar way, the glycation rate of Hb, isolated from diabetic blood and of <SYM98>-2-microglobulin isolated from amyloid plaques from uremic patients was determined The application of MALDI-TOF-MS for in vitro studies revealed important new insights into glycation mechanisms. Whereas the measurement of the intact proteins allows the determination of the average glycation rate, peptide mapping prior to MALDI-TOF-MS can reveal the exact structures of the glycation products and the glycation site. Furthermore, when the unmodified peptide is used as internal standard, MALDI-TOF-MS can also be used for reliable, site specific relative quantification of defined glycation products. REFERENCE COUNT: 83

L1 ANSWER 6 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2004:280711 CAPLUS
DOCUMENT NUMBER: 141:119489
TITLE: Tracking cell signaling protein expression and phosphorylation by innovative proteomic solutions
AUTHOR(S): Pelech, Steven
CORPORATE SOURCE: Department of Medicine, University of British Columbia, Vancouver, BC, Can.
SOURCE: Current Pharmaceutical Biotechnology (2004), 5(1), 69-77
CODEN: CPBUBP; ISSN: 1389-2010
PUBLISHER: Bentham Science Publishers Ltd.
DOCUMENT TYPE: Journal; General Review
LANGUAGE: English
AB A review. The most challenging and fruitful biomedical research endeavor of this decade will be the mapping of cell signaling systems and establishing their linkages to normal and disease-related processes. Amongst other things, the Human Genome Sequencing Project has greatly facilitated MALDI-TOF mass spectrometry identification of proteins that have been resolved by standard 2D gel electrophoresis. However, the low abundance of protein kinases and other signal transduction proteins has rendered their

analyses particularly problematic without some means of purification and enrichment from cell and tissue lysates. Antibodies have been the most specific affinity probes for tracking target proteins, but their variable quality and high cost preclude their deployment in most discovery-based proteomics studies. Current multi-immunoblotting techniques can permit the probing of a single mini-SDS-PAGE gel with 50 or more antibodies at a time to monitor large changes in the expression and phosphorylation states of signaling proteins. The development of new affinity probes to replace antibodies is necessary to drive large scale proteomics studies. Such affinity probes could include short peptide antibody mimetics (PAM's) and oligonucleotide aptamers that when spotted in 2D array formats (e.g. membrane macroarrays, glass microarrays) or presented on specific beads (e.g. Luminex beads) can capture target proteins for their specific enrichment. The bound target proteins can then be detected using reporter antibodies or other specific probes for their quantitation by high throughput systems. These new proteomics methodologies will accelerate assessment of specific protein expression, post-translational modification, protein-protein interactions and protein-drug interactions to provide a more holistic view of cellular operations and how they might be manipulated under pathol. circumstances.
REFERENCE COUNT: 21

L1 ANSWER 12 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2003:940872 CAPLUS
DOCUMENT NUMBER: 141:170319
TITLE: "Qualitative and quantitative proteomics by two-dimensional gel electrophoresis, peptide mass fingerprint and a chemically-coded affinity tag (CCAT)"
AUTHOR(S): *Watt, Steven Alexander; Patschkowski, Thomas; Kalinowski, Jorn; Niehaus, Karsten*
CORPORATE SOURCE: Fakultat fur Biologie, Lehrstuhl fur Genetik, Universitat Bielefeld, Bielefeld, 33501, Germany
SOURCE: **Journal of Biotechnology (2003), 106(2-3), 287-300**
CODEN: JBITD4; ISSN: 0168-1656
PUBLISHER: Elsevier Science B.V.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The chemical-coded affinity tag (CCAT) method combines standard electrophoresis protocols with MALDI-TOF-MS anal. to identify and quantify protein abundances in complex samples in one step. This method is designed to fit into the workflow of SDS-PAGE or two-dimensional electrophoresis (2-DE) only requiring basic proteome laboratory equipment. Prior to electrophoresis two protein samples are sep. labeled with a heavy or a light version of the CCAT reagent via reduced cysteines in the proteins. Equal amts. are then combined and electrophoretically separated Proteins can then be excised from the gel to obtain their peptide mass fingerprint by mass spectrometry. This fingerprint enabled not only identification, but also quantification by comparing relative peak intensities of CCAT-labeled peptides. In this article, we display how the CCAT method can be used to analyze two protein samples in one gel and that the peak intensities of labeled peptides reflect the abundance of a protein in it.
REFERENCE COUNT: 5

L1 ANSWER 14 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2003:857480 CAPLUS
DOCUMENT NUMBER: 140:38365
TITLE: Single-step perfusion chromatography with a throughput potential for enhanced peptide detection by matrix-assisted laser desorption/ionization-mass spectrometry
AUTHOR(S): Choi, Byung-Kwon; Cho, Young-Moon; Bae, Soo-Han; Zoubaulis, Christos C.; Paik, Young-Ki
CORPORATE SOURCE: Department of Biochemistry, Yonsei Proteome Research Center and Biomedical Proteome Research Center, Yonsei University, Seoul, S. Korea
SOURCE: Proteomics (2003), 3(10), 1955-1961
CODEN: PROTC7; ISSN: 1615-9853
PUBLISHER: Wiley-VCH Verlag GmbH & Co. KGaA
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Mass spectrometric peptide mapping of proteins separated by two-dimensional gel electrophoresis can be routinely performed by matrix-assisted laser desorption/ionization mass spectrometry (MALDI-MS) which has become a standard tool. Since MALDI-MS detection relies heavily on the quality of the MALDI target, development of an efficient sample preparation technique for removal of sample contaminants is necessary. To date, among the several sample preparation techniques for MALDI targets available, multistep perfusion chromatog. (MSPC) using Poros R2 and Oligo R3 has been most commonly used. However, MSPC requires at least four working steps and is not efficient for high-throughput anal. and recovery of low abundance proteins. During the course of proteomic anal. of a large set of rat liver tissues and the immortalized human sebaceous gland cells (SZ95 cells), we were interested in developing an alternative to MSPC. Here, we describe a single-step perfusion chromatog. (SSPC) method for MALDI target preparation, which uses a tiny column packed with a mixture of Poros R2 and Oligo R3 resins. The SSPC method significantly improves not only detection of peptides but also efficiency of sample handling, thus enabling high-throughput sample preparation for analyzing large set of samples with high resolution and reproducibility.
REFERENCE COUNT: 19

L1 ANSWER 16 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2003:800837 CAPLUS
DOCUMENT NUMBER: 140:352966
TITLE: Closely spaced external standard: A universal method of achieving 5 ppm mass accuracy over the entire MALDI plate in axial matrix-assisted laser desorption/ionization time-of-flight mass spectrometry
AUTHOR(S): Moskovets, Eugene; Chen, Hsuan-Shen; Pashkova, Anna; Rejtar, Tomas; Andreev, Viktor; Karger, Barry L.
CORPORATE SOURCE: Barnett Institute and Department of Chemistry, Northeastern University, Boston, MA, 02115, USA
SOURCE: Rapid Communications in Mass Spectrometry (2003), 17(19), 2177-2187
CODEN: RCMSEF; ISSN: 0951-4198
PUBLISHER: John Wiley & Sons Ltd.

DOCUMENT TYPE: Journal
LANGUAGE: English
AB Close deposition of the sample and external standard was used in axial matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOFMS) to achieve mass accuracy equivalent to that obtained with an internal standard across the entire MALDI plate. In this work, the sample and external standard were deposited by continuous deposition in sep. traces, each approx. 200 <SYM109>m wide. The dependence of the mass accuracy on the distance between the sample and standard traces was determined across a MALDI target plate with dimensions of 57.5 mm + 57.0 mm by varying the gap between the traces from 100 <SYM109>m to 4 mm. During acquisition, two adjacent traces were alternately irradiated with a 200-Hz laser, such that the peaks in the resulting mass spectra combined the sample and external standard Ion suppression was not observed even when the peptide concns. in the two traces differed by more than two orders of magnitude. The five peaks from the external standard trace were used in a four-term mass calibration of the masses of the sample trace. The average accuracy across the whole plate with this method was 5 ppm when peaks of the sample trace had signal-to-noise ratios of at least 30 and the gap between the traces was approx. 100 <SYM109>m. This approach was applied to determining peptide masses of a reversed-phase liquid chromatog. (LC) separation of a tryptic digest of <SYM98>-galactosidase deposited as a long serpentine trace across the MALDI plate, with accuracy comparable to that obtainable using internal calibration. In addition, the eluent from reversed-phase LC separation of a strong cation-exchange fraction containing tryptic peptides from a yeast lysate along with the closely placed external standard was deposited on the MALDI plate. The data obtained in the MS and MS/MS modes on a MALDI-TOF/TOF mass spectrometer were combined and used in database searching with MASCOT. Since the significant score is a function of mass accuracy in the MS mode, database searching with high mass accuracy reduced the number of false positives and also added peptides which otherwise would have been eliminated at lower mass accuracy (false negatives).
REFERENCE COUNT: 22

L1 ANSWER 18 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2003:512622 CAPLUS
DOCUMENT NUMBER: 140:195780
TITLE: "Analysis of relative isotopologue abundances for quantitative profiling of complex protein mixtures labelled with the acrylamide/D3-acrylamide alkylation tag system"
AUTHOR(S): *Cahill, Michael A.; Wozny, Wojciech; Schwall, Gerhard; Schroer, Klaus; Hoelzer, Kerstin; Poznanovic, Slobodan; Hunzinger, Christian; Vogt, Josef A.; Stegmann, Werner; Matthies, Helmut; Schrattenholz, Andre*
CORPORATE SOURCE: ProteoSys AG, Mainz, 55129, Germany
SOURCE: **Rapid Communications in Mass Spectrometry (2003),17(12), 1283-1290**
CODEN: RCMSEF; ISSN: 0951-4198
PUBLISHER: John Wiley & Sons Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The new method of anal. of relative isotopologue abundances (ARIA) applied here is based on the evaluation of total isotope patterns of tryptic protein fragments measured by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOFMS) to calculate the mixing ratios of composites consisting of stable isotope labeled and isotopically natural (unlabeled) proteins, as described in an accompanying paper in this issue. Recently, Sechi and Gehanne et al. introduced the use of differential quant. mass anal. by MALDI-TOFMS using mixts. of standard proteins alkylated prior to two-dimensional PAGE (2D-PAGE) with either acrylamide (AA) or deuterium-labeled [2,3,3'-D3]-acrylamide (D3AA). In the present study we validate the AA/D3AA system, firstly by measuring the yield of proteins alkylated with AA, and secondly by using differential radioactive labels (125I and 131I) to quant. establish that non-comigration in 2D-PAGE is negligible. ARIA is then applied to quant. estimate the relative proportions of peptides labeled with AA or D3AA in the validated system, using typical silver-stained 2D-PAGE protein spots from 2D gels loaded with 150 <SYM109>g of total liver protein. The precision and limitations of ARIA quantification of peptides differentially alkylated with isotopomeric reagents are discussed. REFERENCE COUNT: 29

L1 ANSWER 19 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2003:509401 CAPLUS
DOCUMENT NUMBER: 140:195623
TITLE: Quantitative analysis of complex peptide reaction systems by mass spectrometry
AUTHOR(S): Weber, Peter J. A.; Chavochi-Negad, Asad; Ghadiri, M. Reza
CORPORATE SOURCE: Institute of Biochemistry, University of Leipzig, Leipzig, 04103, Germany
SOURCE: Peptides 2000, Proceedings of the European Peptide Symposium, 26th, Montpellier, France, Sept. 10-15, 2000 (2001), Meeting Date 2000, 87-88. Editor(s): Martinez, Jean; Fehrentz, Jean-Alain. Editions EDK: Paris, Fr.
CODEN: 69EDWK; ISBN: 2-84254-048-4
DOCUMENT TYPE: Conference
LANGUAGE: English
AB The authors were able to show that the simultaneous quant. MALDI-TOF-MS anal. of up to 16 different peptides is easily achievable by using the novel matrix system TCEP/2-mercaptobenzothiazole (MBT) and a single internal standard.
REFERENCE COUNT: 5

L1 ANSWER 22 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2002:785178 CAPLUS
DOCUMENT NUMBER: 138:86044
TITLE: "A protein molecular weight map of ES2 clear cell ovarian carcinoma cells using a two-dimensional liquid separations/mass mapping technique"
AUTHOR(S): *Wang, Haixing; Kachman, Maureen T.; Schwartz, Donald R.; Cho, Kathleen R.; Lubman, David M.*
CORPORATE SOURCE: Department of Chemistry, School of Medicine, The University of Michigan, Ann Arbor, MI, 48109-1055, USA
SOURCE: **Electrophoresis (2002), 23(18), 3168-3181**
CODEN: ELCTDN; ISSN: 0173-0835

PUBLISHER: Wiley-VCH Verlag GmbH & Co. KGaA
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A mol. weight map of the protein content of ES2 human clear cell ovarian carcinoma cells has been produced using a two-dimensional (2-D) liquid sepns./mass mapping technique. This method uses a 2-D liquid separation of proteins from whole cell lysates coupled online to an electrospray ionization-time of flight (ESI-TOF) mass spectrometer to map the accurate intact mol. weight (Mr) of the protein content of the cells. The two separation dimensions involve the use of liquid isoelec. focusing as the first phase and nonporous silica reversed-phase high-performance liquid chromatog. (HPLC) as the second phase of separation The detection by ESI-TOF-MS provides an image of pl vs. Mr analogous to 2-D gel electrophoresis. Each protein is then identified based upon matrix-assisted laser desorption/ionization (MALDI)-TOF-MS peptide mapping and intact Mr so that a standard map is produced against which other ovarian carcinoma cell lines can be compared. The accurate intact Mr together with the pl fraction, and peptide map serve to tag the protein for future interlysate comparisons. An internal standard is also used to provide a means for quantitation for future interlysate studies. In the ES2 cell line under study it is shown that nearly 900 Mr bands are detected over 17 pl fractions from pH 4 to 12 and a Mr range up to 85 kDa and that around 290 of these bands can be identified using mass spectrometric based techniques. The protein Mr is detected within an accuracy of 150 ppm and it is shown that many of the proteins in this human cancer sample are modified compared to the database. The protein Mr map may serve as a highly reproducible standard Web-based method for comparing proteins from related human cell lines. REFERENCE COUNT: 46

L1 ANSWER 27 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2002:185638 CAPLUS
DOCUMENT NUMBER: 136:213183
TITLE: *Quantitative MALDI-time of flight mass spectrometry of peptides and proteins*
INVENTOR(S): Ammon, Daniel M.
PATENT ASSIGNEE(S): USA
SOURCE: U.S. Pat. Appl. Publ., 45 pp.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2002031773	A1	20020314	US 2001-876412	20010607

PRIORITY APPLN. INFO.: US 2000-210074P P 20000607
AB A method of quant. analyzing a sample analyte involves performing matrix-assisted laser desorption ionization mass spectrometry on the sample analyte and an internal standard, and comparing the mass spectrometry of the sample analyte with the mass spectrometry of the internal standard.

L1 ANSWER 28 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2002:179432 CAPLUS

DOCUMENT NUMBER: 136:291292
TITLE: "A 2-D liquid separations/mass mapping method for interlysate comparison of ovarian cancers"
AUTHOR(S): *Kachman, Maureen T.; Wang, Haixing; Schwartz, Donald R.; Cho, Kathleen R.; Lubman, David M.*
CORPORATE SOURCE: Department of Chemistry and Department of Pathology, School of Medicine, The University of Michigan, Ann Arbor, MI, 48109-1055, USA
SOURCE: **Analytical Chemistry (2002), 74(8), 1779-1791**
CODEN: ANCHAM; ISSN: 0003-2700
PUBLISHER: American Chemical Society
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A two-dimensional liquid phase separation of proteins from whole cell lysates coupled online to an electrospray-ionization time-of-flight (ESI-TOF) mass spectrometer (MS) is used to map the protein content of ovarian surface epithelial cells (OSE) and an ovarian carcinoma-derived cell line (ES2). The two dimensions involve the use of liquid isoelec. focusing as the first phase and nonporous silica reversed-phase HPLC as the second phase of separation Accurate mol. weight (MW) values are then obtained upon the basis of ESI-TOFMS so that an image of isolectric point (pI) vs. MW analogous to 2-D gel electrophoresis is produced. The accurate MW together with the pI fraction and corresponding hydrophobicity (%B) are used to tag each protein so that protein expression can be compared in interlysate studies. Each protein is also identified on the basis of matrix-assisted laser desorption-ionization (MALDI) TOFMS peptide mapping and intact MW so that a standard map is produced against which other cell lines can be compared. Quant. changes in protein expression are measured in these interlysate comparisons using internal stds. in the online ESI-TOFMS process. In the ovarian epithelial cell lines under study, it is shown that in the three pI fractions chosen for detailed anal., over 50 unique proteins can be detected per fraction, of which 40% can be identified from web-based databases. It is also shown that when using an accurate MW to compare proteins in the OSE vs. ovarian cancer sample, there are proteins highly expressed in cancer cells but not in normal cells. In addition, many of the proteins in the cancer sample appear to be down-regulated, as compared to the normal cells. This two-dimensional (2-D) liquid/mass mapping method may provide a means of studying proteins in interlysate comparisons not readily available by other methods.
REFERENCE COUNT: 48

L1 ANSWER 30 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2002:124062 CAPLUS
DOCUMENT NUMBER: 136:332232
TITLE: On-target fraction collection for the off-line coupling of capillary isoelectric focusing with matrix-assisted laser desorption/ionization mass spectrometry
AUTHOR(S): Chartogne, Anne; Gaspari, Marco; Jespersen, Sonja; Buscher, Brigitte; Verheij, Elwin; Van der Heijden, Robert; Tjaden, Ubbo; Van der Greef, Jan
CORPORATE SOURCE: Division of Analytical Chemistry, Leiden/Amsterdam Center for Drug Research, Leiden, 2300 RA, Neth.
SOURCE: Rapid Communications in Mass Spectrometry (2002), 16(3), 201-207

CODEN: RCMSEF; ISSN: 0951-4198
PUBLISHER: John Wiley & Sons Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The authors describe a collection system for the off-line coupling of capillary isoelec. focusing (CIEF) with matrix-assisted laser desorption/ionization time-of-flight (MALDI-TOF) mass spectrometry. In this system, the capillary effluent is directly deposited in fractions onto the MALDI target via the use of a sheath liquid The collected fractions are subsequently supplemented with matrix and further analyzed by MALDI-TOF mass spectrometry for mass assignment. The exptl. set-up includes a fiber optic based UV detector operating at 280 nm, which allows the study of the influence of the sheath liquid composition on the CIEF separation The influence of the carrier ampholyte concentration on the protein MALDI spectra was also evaluated and the feasibility of the collection method was finally demonstrated with a mixture of four standard proteins.
REFERENCE COUNT: 18

L1 ANSWER 36 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2001:105309 CAPLUS
DOCUMENT NUMBER: 134:219101
TITLE: Single molecule detector for mass spectrometry with mass independent detection efficiency
AUTHOR(S): Twerenbold, Damian; Gerber, Daniel; Gritti, Dominique; Gonin, Yvan; Netuschill, Alexandre; Rossel, Frederic; Schenker, Dominique; Vuilleumier, Jean-Luc
CORPORATE SOURCE: Institut de Physique, Universite Neuchatel, Neuchatel, CH-2000, Switz.
SOURCE: Proteomics (2001), 1(1), 66-69 Published in: Electrophoresis, 22(2)
CODEN: PROTC7; ISSN: 1615-9853
PUBLISHER: Wiley-VCH Verlag GmbH
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Exptl. results from equimolar PEG and protein stds. samples are presented from a MALDI-TOF mass spectrometer equipped with both ionizing detectors and the novel single mol. sensitive cryodetectors. The data are consistent with a model hypothesis suggesting that the observed decrease in signal strength in conventional ionizing detector MALDI-TOF mass spectrometers can be explained by the exponentially decreasing quantum efficiency of ionizing detectors. Cryodetectors, in contrast, have a mass independent detection efficiency of 100% on impact and provide addnl. information on the mol. state owing to the calorimetric nature of the detection mechanism.
REFERENCE COUNT: 13

L1 ANSWER 37 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2000:670644 CAPLUS
DOCUMENT NUMBER: 134:159591
TITLE: A microsystem platform interfacing MALDI-TOF MS for high speed automated protein identification

AUTHOR(S): Ekstrom, Simon; Onnerfjord, Patrik; Bengtsson, Martin; Miliotis, Tasso; Ericsson, David; Nilsson, Johan; Marko-Varga, Gyorgy; Laurell, Thomas
CORPORATE SOURCE: Dept. Electrical Measurements, University of Lund, Lund, 221 00, Swed.
SOURCE: Micro Total Analysis Systems 2000, Proceedings of the <SYM109>TAS Symposium, 4th, Enschede, Netherlands, May 14-18, 2000 (2000), 455-458. Editor(s): Van den Berg, Albert; Olthuis, W.; Bergveld, Piet. Kluwer Academic Publishers: Dordrecht, Neth.
CODEN: 69AJPB
DOCUMENT TYPE: Conference
LANGUAGE: English
AB A generic micro chemical and fluidic platform interfacing matrix-assisted laser desorption/ionization time of flight mass spectrometry (MALDI-TOF MS) that facilitates protein anal. is presented. The microsystem comprises a flow-through piezo dispenser, nanovial MALDI- targets and if needed enzyme (protease) activated porous silicon microreactors (<SYM109>-chip IMER) for online digestions of proteins. This microsystem can be used to perform enrichment of low abundant, >1 nM, peptides and proteins from 2-DE, <SYM109>-LC or to perform protein identification through peptide mass mapping. Applications of the system for automated protein identification, sample enrichment and coupling to <SYM109>-LC is demonstrated.
REFERENCE COUNT: 10

L1 ANSWER 38 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2000:538616 CAPLUS
DOCUMENT NUMBER: 133:267137
TITLE: "Quantitation of peptides and proteins by matrix-assisted laser desorption/ionization mass spectrometry using 18O-labeled internal standards"
AUTHOR(S): *Mirgorodskaya, Olga A.; Kozmin, Yuri P.; Titov, Mikhail I.; Korner, Roman; Sonksen, Carsten P.; Roepstorff, Peter*
CORPORATE SOURCE: Institute of Cytology, Russian Academy of Sciences, St. Petersburg, 194064, Russia
SOURCE: **Rapid Communications in Mass Spectrometry (2000), 14(14), 1226-1232**
CODEN: RCMSEF; ISSN: 0951-4198
PUBLISHER: John Wiley & Sons Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A method for quantitating proteins and peptides in the low picomole and sub-picomole range has been developed using matrix-assisted laser desorption/ionization mass spectrometry (MALDI-MS) with internal 18O-labeled stds. A simple procedure is proposed to produce such internal stds. for the tested sample by enzymic hydrolysis of the same sample (with known concentration) in 18O-water. A math. algorithm was developed which uses the isotopic patterns of the substance, the internal standard, and the substance/internal standard mixture for accurate quantitation of the substance. A great advantage of the proposed method is the absence of mol. weight limitation for the protein quantitation and the possibility of quantitation without previous fractionation of proteins and peptides. Using this strategy, the peptide angiotensinogen and two proteins, RNase

and its protein inhibitor, were quantified by MALDI-time-of-flight (TOF) mass spectrometry. REFERENCE COUNT: 18

L1 ANSWER 50 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1997:126941 CAPLUS
DOCUMENT NUMBER: 126:248473
TITLE: "Selection of internal standards for quantitative analysis by matrix-assisted laser desorption-ionization (MALDI) time-of-flight mass spectrometry"
AUTHOR(S): *Wilkinson, William R.; Gusev, Arkady I.; Proctor, Andrew; Houalla, Marwan; Hercules, David M.*
CORPORATE SOURCE: Dep. Chem., Vanderbilt Univ., Nashville, TN, 37235, USA
SOURCE: **Fresenius' Journal of Analytical Chemistry (1997), 357(3), 241-248**
CODEN: FJACES; ISSN: 0937-0633
PUBLISHER: Springer
DOCUMENT TYPE: Journal
LANGUAGE: English
AB For the quantification of bovine insulin, a series of internal stds. was investigated, including horse heart cytochrome c, bovine insulin chain B, des-pentapeptide human insulin, and des-octapeptide porcine insulin. The des-pentapeptide human insulin was the most appropriate internal standard in the range 0.5-0.4 <SYM109>mol/L. Two methods for measuring MALDI signal intensity were evaluated: direct peak integration following subtraction of a linear background and nonlinear least squares curve fitting. The results of both methods were equivalent.

L3 ANSWER 1 OF 24 CAPLUS COPYRIGHT 2004 ACS on STN
TI A Kunitz type protease inhibitor related protein is synthesized in Drosophila prepupal salivary glands and released into the moulting fluid during pupation

L3 ANSWER 2 OF 24 CAPLUS COPYRIGHT 2004 ACS on STN
TI Characterization of Covalent Multimers of Crystallins in Aging Human Lenses

L3 ANSWER 3 OF 24 CAPLUS COPYRIGHT 2004 ACS on STN
TI Integrated sample preparation and MALDI mass spectrometry on a microfluidic compact disk

L3 ANSWER 4 OF 24 CAPLUS COPYRIGHT 2004 ACS on STN
TI Existence of deamidated <SYM97>B-crystallin fragments in normal and cataractous human lenses

L3 ANSWER 5 OF 24 CAPLUS COPYRIGHT 2004 ACS on STN
TI Evaluation of Surface-Protein Binding Constants by Matrix-Assisted Laser Desorption Ionization Mass Spectrometry

L3 ANSWER 6 OF 24 CAPLUS COPYRIGHT 2004 ACS on STN
TI Protein incorporation into MALDI-matrix crystals investigated by high resolution field emission scanning electron microscopy

L3 ANSWER 7 OF 24 CAPLUS COPYRIGHT 2004 ACS on STN
TI The use of paramagnetic probes for determining the structure of proteins

L3 ANSWER 8 OF 24 CAPLUS COPYRIGHT 2004 ACS on STN
TI MALDI/MS-based epitope mapping of antigens bound to immobilized antibodies

L3 ANSWER 9 OF 24 CAPLUS COPYRIGHT 2004 ACS on STN
TI Manipulation of temperature to improve solubility of hydrophobic proteins and cocrystallization with matrix for analysis by MALDI-TOF mass spectrometry

L3 ANSWER 10 OF 24 CAPLUS COPYRIGHT 2004 ACS on STN
TI Crystallization of a recombinant form of the complete sequence of human <SYM103>-interferon: characterization by small-angle X-ray scattering, mass spectrometry and preliminary X-ray diffraction studies

L3 ANSWER 11 OF 24 CAPLUS COPYRIGHT 2004 ACS on STN
TI A modified silver staining protocol for visualization of proteins compatible with matrix-assisted laser desorption/ionization and electrospray ionization-mass spectrometry

L3 ANSWER 12 OF 24 CAPLUS COPYRIGHT 2004 ACS on STN
TI Characterization of crystal content by ESI-MS and MALDI-MS

L3 ANSWER 13 OF 24 CAPLUS COPYRIGHT 2004 ACS on STN
TI Mass Spectrometric Analysis of Mercury Incorporation into Proteins for X-ray Diffraction Phase Determination

L3 ANSWER 14 OF 24 CAPLUS COPYRIGHT 2004 ACS on STN
TI Matrix-Assisted Laser Desorption Ionization Mass Spectrometry: A New Tool for Probing Interactions between Proteins and Metal Surfaces Use in Dental Implantology

L3 ANSWER 15 OF 24 CAPLUS COPYRIGHT 2004 ACS on STN
TI Is the incorporation of analytes into matrix crystals a prerequisite for matrix-assisted laser desorption/ionization mass spectrometry? A study of five positional isomers of dihydroxybenzoic acid

L3 ANSWER 16 OF 24 CAPLUS COPYRIGHT 2004 ACS on STN
TI A comparison of MALDI-MS sample preparation strategies for proteins in complex biological mixtures

L3 ANSWER 17 OF 24 CAPLUS COPYRIGHT 2004 ACS on STN
TI Characterization of the covalent structure of proteins from biological material by MALDI mass spectrometry - possibilities and limitations

L3 ANSWER 18 OF 24 CAPLUS COPYRIGHT 2004 ACS on STN
TI Peptide mass fingerprint sequence coverage from differently stained proteins on two-dimensional electrophoresis patterns by matrix assisted laser desorption/ionization-mass spectrometry (MALDI-MS)

L3 ANSWER 19 OF 24 CAPLUS COPYRIGHT 2004 ACS on STN
TI Investigations of 2,5-DHB and succinic acid as matrixes for UV and IR MALDI. Part II: crystallographic and mass spectrometric analysis

L3 ANSWER 20 OF 24 CAPLUS COPYRIGHT 2004 ACS on STN
TI Hysteresis effects observed in MALDI using oriented, protein-doped matrix crystals

L3 ANSWER 21 OF 24 CAPLUS COPYRIGHT 2004 ACS on STN
TI Protein identification from 2-DE gels by MALDI mass spectrometry

L3 ANSWER 22 OF 24 CAPLUS COPYRIGHT 2004 ACS on STN
TI Ice as a matrix for IR-matrix-assisted laser desorption/ionization: mass spectra from a protein single crystal

L3 ANSWER 23 OF 24 CAPLUS COPYRIGHT 2004 ACS on STN
TI Rapid detection of proteins in body fluids by MALDI/TOFMS - a simple sample preparation for MS

=> d l3 ibib abs 3, 6, 9, 10, 16, 20-23

L3 ANSWER 3 OF 24 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2003:961340 CAPLUS
DOCUMENT NUMBER: 140:124707
TITLE: Integrated sample preparation and MALDI mass spectrometry on a microfluidic compact disk
AUTHOR(S): Gustafsson, Magnus; Hirschberg, Daniel; Palmberg, Carina; Joernvall, Hans; Bergman, Tomas
CORPORATE SOURCE: Gyros AB, Uppsala, SE-751 83, Swed.
SOURCE: Analytical Chemistry (2004), 76(2), 345-350
CODEN: ANCHAM; ISSN: 0003-2700
PUBLISHER: American Chemical Society
DOCUMENT TYPE: Journal
LANGUAGE: English
AB High-throughput microfluidic processing of protein digests integrated with matrix-assisted laser desorption/ionization (MALDI) mass spectrometry on a compact disk (CD) is described. Centrifugal force moves liquid through multiple microstructures, each containing a 10-nL reversed-phase chromatog. column. The CD enables parallel preparation of 96 samples with vols. ranging from one to several microliters. The peptides in the digests are concentrated, desalted, and subsequently eluted from the columns directly into MALDI target areas (200+400 <SYM109>m) on the CD using a solvent containing the MALDI matrix. After crystallization, the CD is inserted into the MALDI instrument for peptide mass fingerprinting and database identification at a routine sensitivity down to the 200-amol level. Detection of proteolytic peptides down to the 50-amol level is demonstrated. The success rate of the CD technol. in protein identification is about twice that of the C18 ZipTips and standard MALDI steel targets. The CDs are operated using robotics to transfer samples and reagents from microcontainers to the processing inlets on the disposable CD and spinning to control the movement of liquid through the microstructures. REFERENCE COUNT: 21

L3 ANSWER 6 OF 24 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2003:163350 CAPLUS
DOCUMENT NUMBER: 139:257632
TITLE: Protein incorporation into MALDI-matrix crystals investigated by high resolution field emission scanning electron microscopy
AUTHOR(S): Horneffer, Verena; Reichelt, Rudolf; Strupat, Kerstin
CORPORATE SOURCE: University of Munster, Institute for Medical Physics and Biophysics, Laser Mass Spectrometry Group, Munster, D-48149, Germany
SOURCE: International Journal of Mass Spectrometry (2003), 226(1), 117-131
CODEN: IMSPF8; ISSN: 1387-3806
PUBLISHER: Elsevier Science B.V.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB In this study, high resolution field emission SEM (FE-SEM) was tested for its feasibility to investigate analyte incorporation into and analyte distribution in slowly grown crystals of 2,5-dihydroxybenzoic acid (2,5-DHB) and 2,6-dihydroxybenzoic acid (2,6-DHB); both compds. function as a matrix for matrix-assisted laser desorption/ionization mass spectrometry (MALDI-MS). To investigate matrix-analyte interaction in 2,5-DHB crystals two Au-labels (20 nm colloidal gold and Nanogold) were examined as potential protein markers to visualize proteins in matrix solids by SEM. For this purpose, analyte-doped 2,5-DHB crystals were mech. cleaved and SEM-micrographs of the opened inner faces were recorded. During the course of the Au-label study, crystal defects became apparent for crystals grown from analyte-free and analyte-doped matrix solns.; these defects are interpreted as fluid or liquid inclusions. The size and amount of liquid inclusions depend on the individual cooling rate during crystal growth and on the size of analyte mols. added to the matrix solution prior to crystal growth. Considering the results obtained for both matrix compds., we assume that analyte incorporation occurs via a solid solution in the case of 2,5-DHB as earlier proposed and not via phase defects such as liquid inclusions. Whether liquid inclusions-presumably filled with saturated mother solution-help to facilitate the desorption/ionization event remains open.REFERENCE COUNT: 51

L3 ANSWER 9 OF 24 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2001:869148 CAPLUS
DOCUMENT NUMBER: 136:50548
TITLE: Manipulation of temperature to improve solubility of hydrophobic proteins and cocrystallization with matrix for analysis by MALDI-TOF mass spectrometry
AUTHOR(S): Bird, Gregory H.; Lajmi, Ajay R.; Shin, Jumi A.
CORPORATE SOURCE: Department of Chemistry, University of Pittsburgh, Pittsburgh, PA, 15260, USA
SOURCE: Analytical Chemistry (2002), 74(1), 219-225
CODEN: ANCHAM; ISSN: 0003-2700
PUBLISHER: American Chemical Society
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Matrix-assisted laser desorption/ionization mass spectrometry (MALDI-MS) requires cocrystn. of analyte with a large excess of matrix, which must be mutually soluble in a solvent that encourages crystal growth upon evaporation MALDI-MS of hydrophobic proteins can be difficult, because they tend to aggregate in polar solns. High concns. of denaturants and salts are often employed to combat protein aggregation, but this can result in signal suppression. By using various organic cosolvent systems and matrixes at different protein:matrix ratios, we were able to use MALDI-TOFMS to detect four bacterially expressed hydrophobic proteins comprising alanine-rich mutants of the basic region/leucine zipper protein (bZIP) GCN4. By manipulating sample temperature, we were able to maintain protein solubility Protein aggregation was suppressed when mixing the protein and matrix solns. at 4° prior to warming to 37°, following the temperature-leap technique described by Xie and Wetlaufer (Protein Sci. 1996, 5, 517-523), who used this method to renature bovine carbonic anhydrase II. Manipulation of temperature encouraged our hydrophobic proteins to adopt conformations leading to the

nonaggregating state, and solubility was maintained even when the concentration of denaturant was reduced from 4 M to 400 mM. The temperature-leap tactic was critical for maintaining protein solubility, preventing signal suppression normally seen with higher concns. of salts, allowing for generation of superior spectra, and should prove applicable to other systems prone to aggregation. REFERENCE COUNT: 46

L3 ANSWER 16 OF 24 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1999:15309 CAPLUS
DOCUMENT NUMBER: 130:248899
TITLE: A comparison of MALDI-MS sample preparation strategies for proteins in complex biological mixtures
AUTHOR(S): Westman, Ann; Karlsson, Gosta; Ekman, Rolf
CORPORATE SOURCE: Institute of Clinical Neuroscience, Department of Psychiatry and Neurochemistry, Sahlgrenska Hospital/Molndal, Goteborg University, Moelndal, S-431 80, Swed.
SOURCE: Advances in Mass Spectrometry (1998), 14,B061950/1-B061950/16
CODEN: AMSPAH; ISSN: 0568-000X
PUBLISHER: Elsevier Science B.V.
DOCUMENT TYPE: Journal; (computer optical disk)
LANGUAGE: English
AB In this study the effects of different sample preparation parameters, e.g., crystallization speed, solvent composition and pH, on matrix-assisted laser desorption/ionization mass spectrometry on complex biol. mixts. are investigated. Descriptions of the implemented sample preparation techniques and the homogeneity, signal-to-noise ratio, and peak widths of mass spectra from proteins added to the naturally occurring in human cerebrospinal fluid are presented. Mass spectra of naturally occurring proteins at concns. less than 100 fmol/<SYM109>L in cerebrospinal fluid are presented. REFERENCE COUNT: 6

L3 ANSWER 21 OF 24 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1997:797221 CAPLUS
DOCUMENT NUMBER: 128:112425
TITLE: Protein identification from 2-DE gels by MALDI mass spectrometry
AUTHOR(S): Jungblut, Peter; Thiede, Bernd
CORPORATE SOURCE: Proteinanalysis, Max-Planck-Institute for Infectionbiology, Berlin, D-10117, Germany
SOURCE: Mass Spectrometry Reviews (1997), 16(3), 145-162
CODEN: MSRVD3; ISSN: 0277-7037
PUBLISHER: John Wiley & Sons, Inc.
DOCUMENT TYPE: Journal; General Review
LANGUAGE: English
AB A review with 149 refs. Two-dimensional electrophoresis (2-DE) allows the separation of proteins at the level of protein species, which are defined by their chemical structure. Each chemical modification leads to a new protein species. Prerequisites for investigations of protein species are reproducible sample preparation, large gels (20 + 30 cm and larger), high sensitive detection methods, automated evaluation of gels, and

sensitive methods for identification of 2-DE-separated protein species. MALDI mass spectrometry with its sensitivity in the fmol range fits with the sensitivity of protein detection on 2-De gels. Protein mass determination, peptide mass mapping, post-source decay sequencing, and ladder sequencing by MALDI-MS in combination with genome databases have the potential for complete structural investigation on the protein species level. The discrimination of 19 crystalline species of mouse eye lens and of 54 human heart heat-shock protein 27 species shows the capacity of the combination of 2-DE with MALDI-MS. REFERENCE COUNT: 149

L3 ANSWER 22 OF 24 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1996:421227 CAPLUS
DOCUMENT NUMBER: 125:109373
TITLE: Ice as a matrix for IR-matrix-assisted laser desorption/ionization: mass spectra from a protein single crystal
AUTHOR(S): Berkenkamp, Stefan; Karas, Michael; Hillenkamp, Franz
CORPORATE SOURCE: Inst. Medical Physics Biophysics, Univ. Muenster, Muenster, D-48149, Germany
SOURCE: Proceedings of the National Academy of Sciences of the United States of America (1996), 93(14), 7003-7007
CODEN: PNASA6; ISSN: 0027-8424
PUBLISHER: National Academy of Sciences
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Lasers emitting in the UV wavelength range of 260-360 nm are almost exclusively used for matrix-assisted laser desorption/ionization mass spectrometry (MALDI-MS) of macromols. Reports about the use of lasers emitting in the IR first appeared in 1990/1991. In contrast to MALDI in the UV, a very limited number of reports on IR-MALDI have since been published. Several matrixes have been identified for IR MALDI yielding spectra of a quality comparable to those obtained in the UV. Water (ice) was recognized early as a potential matrix because of its strong O-H stretching mode near 3 <SYM109>m. Interest in water as matrix derives primarily from the fact that it is the major constituent of most biol. tissues. If functional as matrix, it might allow the in situ anal. of macromol. constituents in frozen cell sections without extraction or exchanging the water. We present results that show that IR-MALDI of lyophilized proteins, air dried protein solns., or protein crystals up to a mol. mass of 30 kDa is possible without the addition of any sep. matrix. Samples must be frozen to retain a sufficient fraction of the water of hydration in the vacuum. The limited current sensitivity, requiring at least 10 pmol of protein for a successful anal. needs to be be further improved.

L3 ANSWER 23 OF 24 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1995:1000915 CAPLUS
DOCUMENT NUMBER: 124:49902
TITLE: Rapid detection of proteins in body fluids by MALDI/TOFMS - a simple sample preparation for MS
AUTHOR(S): Kishikawa, Masahiko; Nakanishi, Toyofumi; Shimizu, Akira

CORPORATE SOURCE: Department of Clinical Pathology, Osaka Medical College, Japan
SOURCE: Nippon Iyo Masu Supekutoru Gakkai Koenshu (1995), 20, 197-200
CODEN: NIMKEN; ISSN: 0916-085X
PUBLISHER: Nippon Iyo Masu Supekutoru Gakkai
DOCUMENT TYPE: Journal
LANGUAGE: Japanese
AB When the authors analyze proteins in body fluids by MALDI/TOFMS salts and coexisting proteins decrease the sensitivity and resolution as well as crystallization of the matrix-sample complex on the target. The authors propose three kinds of sample prepns. for detection of proteins in serum and urine by MALDI/TOFMS. First, by only dilution with distilled water to 10-150 times, albumin and the incomplete Ig heavy chain in globin and lysozyme in urine from patients with nephritis, monoclonal gammopathy and monocytic leukemia were clearly detected. Second, adsorption of albumin with Blue gel or IgG with Protein G Sepharose 4FF could improve the sensitivity and resolution when the signals are superimposed by high levels of coexistence such as with albumin and IgG. This procedure may practically be applied for the rapid diagnosis of these diseases. Finally, by immunopptn. with specific antisera, proteins at lower concns., such as carbohydrate deficient transferrin, could be detected with good resolution.

L6 ANSWER 1 OF 2 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1999:745332 CAPLUS
DOCUMENT NUMBER: 131:359695
TITLE: A novel interface for on-line coupling of liquid capillary chromatography with matrix-assisted laser desorption/ionization detection
AUTHOR(S): Zhan, Qiao; Gusev, Arkady; Hercules, David M.
CORPORATE SOURCE: Department of Chemistry, Vanderbilt University, Nashville, TN, 37235, USA
SOURCE: Rapid Communications in Mass Spectrometry (1999), 13(22), 2278-2283
CODEN: RCMSEF; ISSN: 0951-4198
PUBLISHER: John Wiley & Sons Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A novel interface was developed which should allow the direct online coupling of liquid capillary chromatog. with matrix-assisted laser desorption/ionization (MALDI) mass spectrometry detection. The interface employs continuous analyte/matrix co-crystallization onto a porous frit installed at a capillary end which was used as the target for MALDI. After separation, the analyte effluent is premixed with the MALDI matrix solution and introduced into the interface. The analyte/matrix mixture is co-crystallized onto the frit surface in the vacuum environment of the mass spectrometer. Continuous matrix/analyte crystallization and interface regeneration is accomplished by a combination of solvent flushing and laser ablation. The memory effect is negligible over a dynamic range of .apprx.200. Several applications, including anal. of small peptides and combination with gel permeation chromatog. (GPC), indicated that the online MALDI interface does not sacrifice chromatog. or mass spectral resolution, and demonstrated the possibility of a reliable LC-MALDI system.

REFERENCE COUNT: 26

L6 ANSWER 2 OF 2 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1999:136422 CAPLUS
DOCUMENT NUMBER: 130:329246
TITLE: Matrix-assisted laser desorption/ionization time-of-flight/thin layer chromatography/mass spectrometry. A rapid method for impurity testing
AUTHOR(S): Mowthorpe, Siew; Clench, Malcolm R.; Cricelius, Anna; Richards, Don S.; Parr, Vic; Tetler, Lee W.
CORPORATE SOURCE: Division of Chemistry, School of Science and Mathematics, Sheffield Hallam University, Sheffield, S1 1WB, UK
SOURCE: Rapid Communications in Mass Spectrometry (1999), 13(4), 264-270
CODEN: RCMSEF; ISSN: 0951-4198
PUBLISHER: John Wiley & Sons Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Thin-layer chromatog./matrix-assisted laser desorption/ionization mass spectrometry (TLC/MALDI-MS) has been previously used to obtain mass spectra from a variety of compds., principally peptides. For pharmaceuticals, which are often of relatively low mol. weight compds., it is important that any matrix materials employed do not interfere with the mass spectra obtained. The key step to successful TLC/MALDI - MS is hence the preparation of the TLC plate prior to mass spectrometry. Crucial to this is the deposition of matrix material into the plate to promote co-crystallization with the analyte. In this work we examined the literature methods for plate preparation and developed 2 new approaches. The first involves brushing the TLC plate with a supersatd. solution of matrix and the second involves electrospraying the TLC plate with a matrix solution Data are presented from the direct anal. of tetracycline and its impurities. Using the electrospray method the limit of detection for tetracycline is 1 ng from a TLC plate. A com. MALDI-TOF mass spectrometer was modified to allow the acquisition of chromatog. data from TLC plates. Chromatograms from replicate spots of 100 and 1 <SYM109>g of tetracycline are shown. REFERENCE COUNT: 15

FILE 'CAPLUS' ENTERED AT 18:18:16 ON 07 OCT 2004
L1 21 ((ISOFORM? OR ISOMER?) (6A) (PROTEIN? OR POLYPEPTID? OR PEPTID?)) (S) MALDI

L1 ANSWER 1 OF 21 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2004:414742 CAPLUS
DOCUMENT NUMBER: 140:402855
TITLE: Quantitative analysis of protein isoforms using matrix-assisted laser desorption/ionization time of flight mass spectrometry
INVENTOR(S): Perryman, M. Benjamin; Helmke, Steve M.; Duncan, Mark W.
PATENT ASSIGNEE(S): The Regents of the University of Colorado, A Body Corporate, USA
SOURCE: PCT Int. Appl., 68 pp.
CODEN: PIXXD2

DOCUMENT TYPE: Patent
PATENT NO. KIND DATE APPLICATION NO. DATE
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WO 2004042072 A2 20040521 WO 2003-US34386 20031030
WO 2004042072 C2 20040826
US 2004119010 A1 20040624 US 2003-697991 20031030
PRIORITY APPLN. INFO.: US 2002-423019P P 20021101
US 2002-423142P P 20021102
AB The present invention provides for methods of quantitating the amts. of proteins or peptides, including those that are closely related isoforms, using matrix-assisted laser desorption/ionization time of flight mass spectrometry (MALDI-TOF-MS). Measurement of protein concns. in vivo has been extremely difficult and problematic, and protein concns. have not been shown to correlate well with mRNA levels, the standard used in the past. The present invention overcomes the deficiencies of prior methodologies by taking advantage of MALDI-TOF-MS technol. and applying it to proteins and peptides in a way that allows for accurate, quant. measurement in vivo of protein or peptide concns.

L1 ANSWER 2 OF 21 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2004:125078 CAPLUS
DOCUMENT NUMBER: 140:249527
TITLE: "Simultaneous quantification of human cardiac <SYM97>- and <SYM98>-myosin heavy chain proteins by MALDI-TOF mass spectrometry"
AUTHOR(S): *Helmke, Steve M.; Yen, Chia-Yu; Cios, Krzysztof J.; Nunley, Karin; Bristow, Michael R.; Duncan, Mark W.; Perryman, M. Benjamin*
CORPORATE SOURCE: Proteomics Facility, Box C-238, and Department of Medicine, Division of Cardiology, University of Colorado Health Sciences Center, Denver, CO, 80262, USA
SOURCE: **Analytical Chemistry (2004), 76(6), 1683-1689**
CODEN: ANCHAM; ISSN: 0003-2700
PUBLISHER: American Chemical Society
DOCUMENT TYPE: Journal
LANGUAGE: English
AB We have developed a novel method for quantifying protein isoforms, in both relative and absolute terms, based on MALDI -TOF mass spectrometry. The utility of the approach is demonstrated by quantifying the <SYM97> and <SYM98> protein isoforms of myosin heavy chain (MyHC) in human atrial tissue. <SYM97>-MyHC (726-741) and <SYM98>-MyHC (724-739) were identified as isoform-specific tryptic peptides. A calibration curve was constructed by plotting ion current ratios against molar ratios of the two peptides prepared synthetically. MyHC was digested by trypsin and the ion current ratio determined for the two tryptic peptides. The ion current ratio was converted to the peptide ratio and hence the isoform ratio by reference to the standard curve. The accuracy of the method was confirmed by a comparison between these results and those determined by an established method of MyHC isoform ratio determination So that the molar ratio could be converted to absolute values, a third peptide, an analog of the two peptides being measured, was synthesized for use as an internal standard (IS). The measured ion current ratios of synthetic <SYM97>-MyHC (726-741), <SYM98>-MyHC

(724-739), and IS peptides were used to generate standard curves. A known quantity of the IS was added to the MyHC digests. The measured ion current ratios were converted to the actual quantities of the isoform-specific peptides and hence the actual quantity of each protein isoform by reference to the standard curves. This method is of general applicability, especially when isoform quantification is required.
REFERENCE COUNT: 29

L1 ANSWER 3 OF 21 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2003:775694 CAPLUS
DOCUMENT NUMBER: 139:361082
TITLE: A method for the detection of asparagine deamidation and aspartate isomerization of proteins by MALDI/TOF-mass spectrometry using endoproteinase Asp-N
AUTHOR(S): Kameoka, Daisuke; Ueda, Tadashi; Imoto, Taiji
CORPORATE SOURCE: Graduate School of Pharmaceutical Sciences, Kyushu University, Fukuoka, 812-8582, Japan
SOURCE: Journal of Biochemistry (Tokyo, Japan) (2003), 134(1), 129-135
CODEN: JOBIAO; ISSN: 0021-924X
PUBLISHER: Japanese Biochemical Society
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A method was established for evaluating Asn deamidation and As isomerization/ racemization. To detect the subtle changes in mass that accompany these chemical modifications, we used a combination of enzyme digestion by endoproteinase Asp-N, which selectively cleaves the N-terminus of L-<SYM97>-Asp, and MALDI/TOF-mass spectrometry. To achieve better resolution, we employed digests of 15N-labeled protein as an internal standard To demonstrate the advantages of this method, we applied it to identify deamidated sites in mutant lysozymes in which the Asn residue is mutated to Asp. We also identified the deamidation or isomerization site of the lysozyme samples after incubating them under acidic or basic conditions. REFERENCE COUNT: 27

L1 ANSWER 7 OF 21 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2003:163353 CAPLUS
DOCUMENT NUMBER: 139:257511
TITLE: Sample preparation protocols for MALDI-MS of peptides and oligonucleotides using prestructured sample supports
AUTHOR(S): Nordhoff, Eckhard; Schurenberg, Martin; Thiele, Gabriela; Lubbert, Christine; Kloeppel, Klaus-Dieter; Theiss, Dorothea; Lehrach, Hans; Gobom, Johan
CORPORATE SOURCE: Scienion AG, Berlin, 12489, Germany
SOURCE: International Journal of Mass Spectrometry (2003), 226(1), 163-180
CODEN: IMSPF8; ISSN: 1387-3806
PUBLISHER: Elsevier Science B.V.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB This contribution provides a set of protocols for MALDI-MS sample preparation of peptides and oligonucleotides on prestructured sample supports. The protocols have been

optimized for high detection sensitivity, robust performance, ease of use, and include sample purification and concentration Some protocols were optimized for manual preparation of individual samples. Others were developed for the use of automated pipetting stations and optimized for high throughput protein identification and DNA sequence anal. REFERENCE COUNT: 29

L1 ANSWER 8 OF 21 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2002:499695 CAPLUS
DOCUMENT NUMBER: 137:197275
TITLE: Secondary and Quaternary Structures of the (+)-Pinoresinol-Forming Dirigent Protein
AUTHOR(S): Halls, Steven C.; Lewis, Norman G.
CORPORATE SOURCE: Institute of Biological Chemistry, Washington State University, Pullman, WA, 99164-6340, USA
SOURCE: Biochemistry (2002), 41(30), 9455-9461
CODEN: BICHAW; ISSN: 0006-2960
PUBLISHER: American Chemical Society
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The (+)-pinoresinol-forming dirigent protein is the first protein capable of stereoselectively coupling two coniferyl alc. derived radical species, in this case to give the 8-8' linked (+)-pinoresinol. Only dimeric cross-linked dirigent protein structures were isolated when 1-ethyl-3-[3-(dimethylamino)-propyl]carbodiimide was used as crosslinking agent, whereas the associated oxidase, presumed to generate the corresponding free radical substrate, was not detected. Native Forsythia intermedia dirigent protein isoforms were addnl. subjected to MALDI-TOF and ESI-MS analyses, which established the presence of both monomeric masses of 23-25 kDa and dimeric dirigent protein species ranging from 46 to 49 kDa. Anal. ultracentrifugation, sedimentation velocity, and sedimentation equilibrium analyses of the native dirigent protein in open solution confirmed further its dimeric nature as well as a propensity to aggregate, with the latter being dependent upon both temperature and solution ionic strength. CD anal. suggested that the dirigent protein was primarily composed of <SYM98>-sheet and loop structures. REFERENCE COUNT: 34

L1 ANSWER 9 OF 21 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2002:495781 CAPLUS
DOCUMENT NUMBER: 137:228554
TITLE: Phenotypic subunit composition of the tobacco (Nicotiana tabacum L.) vacuolar-type H+-translocating ATPase
AUTHOR(S): Drobny, Martina; Schnolzer, Martina; Fiedler, Sabine; Luttge, Ulrich; Fischer-Schliebs, Elke; Christian, Anna-Luise; Ratajczak, Rafael
CORPORATE SOURCE: Institute of Botany, Darmstadt University of Technology, Darmstadt, D-64287, Germany
SOURCE: Biochimica et Biophysica Acta (2002), 1564(1), 243-255
CODEN: BBACAQ; ISSN: 0006-3002
PUBLISHER: Elsevier Science B.V.

DOCUMENT TYPE: Journal
LANGUAGE: English
AB The model plant tobacco (Nicotiana tabacum L.) was chosen for a survey of the subunit composition of the V-ATPase at the protein level. V-ATPase was purified from tobacco leaf cell tonoplasts by solubilization with the nonionic detergent Triton X-100 and immunopptn. In the purified fraction 12 proteins were present. By matrix-assisted laser-desorption ionization mass spectrometry (MALDI-MS) and amino acid sequencing 11 of these polypeptides could be identified as subunits A, B, C, D, F, G, c, d and three different isoforms of subunit E. The polypeptide which could not be identified by MALDI anal. might represent subunit H. The data presented here, for the first time, enable an unequivocal identification of V-ATPase subunits after gel electrophoresis and open the possibility to assign changes in polypeptide composition to variations in resp. V-ATPase subunits occurring as a response to environmental conditions or during plant development. REFERENCE COUNT: 71

L1 ANSWER 10 OF 21 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2002:465331 CAPLUS
DOCUMENT NUMBER: 137:167573
TITLE: Identification of oxidized plasma proteins in Alzheimer's disease
AUTHOR(S): Choi, Joungil; Malakowsky, Christina A.; Talent, John M.; Conrad, Craig C.; Gracy, Robert W.
CORPORATE SOURCE: Molecular Aging Unit, Department of Molecular Biology and Immunology, Health Science Center, University of North Texas, Fort Worth, TX, 76107, USA
SOURCE: Biochemical and Biophysical Research Communications (2002), 293(5), 1566-1570
CODEN: BBRCA9; ISSN: 0006-291X
PUBLISHER: Elsevier Science
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The modification of proteins by reactive oxygen species is central to the pathol. of Alzheimer's disease (AD). Previously, we have observed specific oxidized proteins in blood plasma of AD subjects. Plasma from AD subjects and age-matched controls was subjected to two-dimensional gel electrophoresis (2-DE). Oxidized proteins with new carbonyl groups were detected by reaction with 2,4-dinitrophenylhydrazine, followed by Western blotting with anti-DNP antibody. Seven principal oxidized protein spots (isoelec. point=4.7-5.5; mol. mass=45-65 kDa) were observed, with varying levels of oxidation in plasma samples from both AD and non-AD subjects. Matrix-assisted laser desorption mass spectroscopy (MALDI -TOF/MS) revealed that these oxidized proteins were isoforms of fibrinogen <SYM103>-chain precursor protein and of <SYM97>-1-antitrypsin precursor. These proteins exhibited a two- to sixfold greater specific oxidation index in plasma from AD subjects when compared to controls. Both these proteins have been previously implicated in the pathol. of the disease. It is possible that oxidized isoforms of these proteins may serve as biomarkers for AD.
REFERENCE COUNT: 42

L1 ANSWER 11 OF 21 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2002:181810 CAPLUS
DOCUMENT NUMBER: 136:399076
TITLE: PKC <SYM101> is associated with myosin IIA and actin in fibroblasts
AUTHOR(S): England, Karen; Ashford, David; Kidd, Daniel; Rumsby, Martin
CORPORATE SOURCE: Department of Biology, University of York, York, YO10 5DD, UK
SOURCE: Cellular Signalling (2002), 14(6), 529-536
CODEN: CESIEY; ISSN: 0898-6568
PUBLISHER: Elsevier Science Inc.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Proteins coimmunopptg. with protein kinase C isoform <SYM101> (PKC-<SYM101>) in fibroblasts were identified through MALDI-TOF mass spectrometry. This method identified myosin IIA in PKC-<SYM101> immunoppts., as well as known PKC-<SYM101>-binding proteins, actin, <SYM98>'Cop, and cytokeratin. Myosin was not a substrate for PKC-<SYM101>. Immunofluorescence anal. showed that PKC-<SYM101> was colocalized with actin and myosin in actomyosin stress fibers in fibroblasts. Inhibitors of PKC and myosin ATPase activity, as well as microfilament-disrupting drugs, all inhibited the spreading of fibroblasts after passage, suggesting a role for a PKC-<SYM101>·actin·myosin complex in cell spreading.
REFERENCE COUNT: 38

L1 ANSWER 12 OF 21 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2002:154221 CAPLUS
DOCUMENT NUMBER: 136:320981
TITLE: Chemical characterization of the lectin from Amaranthus leucocarpus syn. hypochondriacus by 2-D proteome analysis
AUTHOR(S): Hernandez, Pedro; Debray, Henri; Jaekel, Heidi; Garfias, Yonathan; Del Carmen Jimenez, Maria; Martinez-Cairo, Salvador; Zenteno, Edgar
CORPORATE SOURCE: Departamento de Bioquimica, Instituto Nacional de Enfermedades Respiratorias, Mexico, 14080, Mex.
SOURCE: Glycoconjugate Journal (2002), Volume Date 2001, 18(4), 321-329
CODEN: GLJOEW; ISSN: 0282-0080
PUBLISHER: Kluwer Academic Publishers
DOCUMENT TYPE: Journal
LANGUAGE: English
AB In this work, the N-acetyl-D-galactosamine specific lectin from Amaranthus leucocarpus syn hypochondriacus (ALL) was characterized. It is a dimeric glycoprotein composed by three isoforms with pl at 4.8, 4.9, and 5.2. CD anal. indicated that the secondary structure of ALL contains 45% of <SYM98>-sheet and 5% of <SYM97>-helix. Amino acid sequence of the purified lectin and its isoforms was determined from peptides obtained after trypsin digestion by MALDI-TOF (matrix-assisted laser desorption ionization-time of flight). The tryptic peptides prepared from the purified lectin and the three isoforms showed different degrees (80 to 83%) of identity with the amino acid sequence belonging to a previously described high nutritional value protein

from A. hypochondriacus not shown at the time to be a lectin. Furthermore, anal. of tryptic peptides obtained from ALL previously treated with peptide N-glycosidase, revealed a 93% identity with the aforementioned protein. Presence of N-glycosidically linked glycans of the oligomannosidic type and, in minor proportion, of the N-acetyllactosaminic type glycans was determined by affinity chromatog. on immobilized Con A. REFERENCE COUNT: 36

L1 ANSWER 13 OF 21 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2002:114358 CAPLUS
DOCUMENT NUMBER: 136:321495
TITLE: "A programmable fragmentation analysis of proteins by in-source decay in MALDI-TOF mass spectrometry"
AUTHOR(S): *Gao, Jialing; Tsugita, Akira; Takayama, Mitsuo; Xu, Lin*
CORPORATE SOURCE: Proteomics Laboratory, Amakubo, Tsukuba, Japan
SOURCE: **Analytical Chemistry (2002), 74(6), 1449-1457**
CODEN: ANCHAM; ISSN: 0003-2700
PUBLISHER: American Chemical Society
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Here we describe an algorithm for identifying peptides/proteins of known sequence and unknown peptides from partial spectra generated by an in-source decay (ISD) technique coupled with matrix-assisted laser desorption/ionization time-of-flight mass spectrometry. The identification of protein fragments is processed with a software program called CMATCH, which generates candidate subsequences for both known peptides/proteins and unknown peptides for the major product ions in the spectral range m/z 400-5000 and then matches these to known protein sequences contained in a reference database for the known peptides/proteins. CMATCH, which is compiled for MSDOS or WINDOWS95/NT, has two main advantages: first, the candidate subsequences are generated automatically without the need for supplementary information concerning the distribution of either N-terminal or C-terminal ions in the spectra for both known peptides/proteins and unknown peptides; second, the highest coordinated homologous sequences are picked up automatically from the reference database as the best matches with known peptides/proteins. Examples from the ISD spectra of several test proteins demonstrate the efficacy of this protein identification software. REFERENCE COUNT: 26

L1 ANSWER 14 OF 21 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2001:884112 CAPLUS
DOCUMENT NUMBER: 136:196015
TITLE: Purification and properties of Arabidopsis thaliana type 1 protein phosphatase (PP1)
AUTHOR(S): Stubbs, Michael D.; Tran, Hue T.; Atwell, Adrian J.; Smith, Catherine S.; Olson, Doug; Moorhead, Greg B. G.
CORPORATE SOURCE: Department of Biological Sciences, University of Calgary, Calgary, AB, T2N 1N4, Can.
SOURCE: Biochimica et Biophysica Acta (2001), 1550(1), 52-63

CODEN: BBACAQ; ISSN: 0006-3002
PUBLISHER: Elsevier Science B.V.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The Arabidopsis thaliana type 1 protein phosphatase (PP1) catalytic subunit was released from its endogenous regulatory subunits by ethanol precipitation and purified by anion exchange and microcystin affinity chromatog. The enzyme was identified by MALDI-TOF mass spectrometry from a tryptic digest of the purified protein as a mixture of PP1 isoforms (TOPP 1-6) indicating that at least 4-6 of the eight known PP1 proteins are expressed in sufficient quantities for purification from A. thaliana suspension cells. The enzyme had a final specific activity of 8950 mU/mg using glycogen phosphorylase a as substrate, had a subunit mol. mass of 35 kDa as determined by SDS-PAGE and behaved as a monomeric protein of approx. 39 kDa on Superose 12 gel filtration chromatog. Similar to the mammalian type 1 protein phosphatases, the A. thaliana enzyme was potently inhibited by Inhibitor-2 (IC50=0.65 nM), tautomycin (IC50=0.06 nM), microcystin-LR (IC50=0.01 nM), nodularin (IC50=0.035 nM), calyculin A (IC50=0.09 nM), okadaic acid (IC50=20 nM) and cantharidin (IC50=60 nM). The enzyme was also inhibited by fostriecin (IC50=22 <SYM109>M), NaF (IC50=2.1 mM), Pi (IC50=9.5 mM), and PPi (IC50=0.07 mM). Purification of the free catalytic subunit allowed it to be used to probe protein phosphatase holoenzyme complexes that were enriched on Q-Sepharose and a microcystin-Sepharose affinity matrix and confirmed several proteins to be PP1 targeting subunits. REFERENCE COUNT: 36

L1 ANSWER 15 OF 21 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2000:860461 CAPLUS
DOCUMENT NUMBER: 134:128063
TITLE: A modified silver staining protocol for visualization of proteins compatible with matrix-assisted laser desorption/ionization and electrospray ionization-mass spectrometry
AUTHOR(S): Yan, Jun X.; Wait, Robin; Berkelman, Tom; Harry, Rachel A.; Westbrook, Jules A.; Wheeler, Colin H.; Dunn, Michael J.
CORPORATE SOURCE: Department of Cardiothoracic Surgery, National Heart and Lung Institute, Imperial College School of Medicine, Heart Science Center, Harefield Hospital, Harefield, UB9 6JH, UK
SOURCE: Electrophoresis (2000), 21(17), 3666-3672
CODEN: ELCTDN; ISSN: 0173-0835
PUBLISHER: Wiley-VCH Verlag GmbH
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The growing availability of genomic sequence information, together with improvements in anal. methodol., have enabled high throughput, high sensitivity protein identification. Silver staining remains the most sensitive method for visualization of proteins separated by two-dimensional gel electrophoresis (2-D PAGE). Several silver staining protocols have been developed which offer improved compatibility with subsequent mass spectrometric anal. We describe a modified silver staining method that is available as a com. kit (Silver Stain PlusOne; Amersham Pharmacia Biotech,

Amersham, UK). The 2-D patterns attained with this modified protocol are comparable to those from other silver staining methods. Omitting the sensitizing reagent allows higher loading without saturation, which facilitates protein identification and quantitation. We show that tryptic digests of proteins visualized by the modified stain afford excellent mass spectra by both matrix-assisted laser desorption/ionization and tandem electrospray ionization. We conclude that the modified silver staining protocol is highly compatible with subsequent mass spectrometric anal.
REFERENCE COUNT: 25

L1 ANSWER 16 OF 21 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2000:819678 CAPLUS
DOCUMENT NUMBER: 134:68405
TITLE: Use of non-porous reversed-phase high-performance liquid chromatography for protein profiling and isolation of proteins induced by temperature variations for Siberian permafrost bacteria with identification by matrix-assisted laser desorption/ ionization time-of-flight mass spectrometry and capillary electrophoresis-electrospray ionization mass spectrometry
AUTHOR(S): Chong, Bathsheba E.; Kim, Jeongkwon; Lubman, David M.; Tiedje, James M.; Kathariou, Sohpia
CORPORATE SOURCE: Department of Chemistry, The University of Michigan, Ann Arbor, MI, 48109-1055, USA
SOURCE: Journal of Chromatography, B: Biomedical Sciences and Applications (2000), 748(1), 167-177
CODEN: JCBBEP; ISSN: 0378-4347
PUBLISHER: Elsevier Science B.V.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Non-porous reversed-phase high-performance liquid chromatog. (NP-RP-HPLC) has been used to sep. and isolate proteins from whole cell lysates of ED 7-3, a bacterium from the buried Siberian permafrost sediment. The proteins collected from the liquid eluent of this separation were then analyzed by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF-MS) and capillary electrophoresis-electrospray ionization mass spectrometry (CE-ESI-MS). In order to study the differences in expression of cold-shock proteins (CSPs) at different growth temps., cultures of the ED 7-3 strain were prepared at 4° and 25°. The goals of this work were twofold: firstly, to identify the presence of CSPs and other proteins that are highly expressed at 4° but not at 25°; and secondly, to isolate these proteins for MALDI-TOF-MS and CE-ESI-MS identification. In this initial work, distinct protein profiles were observed for these cultures as a function of temperature Fraction collection from the eluent of NP-RP-HPLC of some of the highly expressed proteins was performed and the proteins were mass analyzed for mol. mass. Peptide maps of the proteins were generated by tryptic digestion and were analyzed by CE-ESI-MS and MALDI-TOF-MS for database identification of the expressed proteins. REFERENCE COUNT: 43

L1 ANSWER 17 OF 21 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2000:661048 CAPLUS

DOCUMENT NUMBER: 134:68258
TITLE: N-Glycan Analysis by Matrix-Assisted Laser Desorption/Ionization Mass Spectrometry of Electrophoretically Separated Nonmammalian Proteins: Application to Peanut Allergen Ara h 1 and Olive Pollen Allergen Ole e 1
AUTHOR(S): Kolarich, Daniel; Altmann, Friedrich
CORPORATE SOURCE: Glycobiology Division, Institute of Chemistry, Universitat fur Bodenkultur Wien, Vienna, Austria
SOURCE: Analytical Biochemistry (2000), 285(1), 64-75
CODEN: ANBCA2; ISSN: 0003-2697
PUBLISHER: Academic Press
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A method has been developed which allows the anal. of glycoproteins separated by SDS-PAGE. The procedure, though applicable to N-glycosylated glycoproteins of any origin, is particularly devised for glycoproteins potentially containing fucose in <SYM97>1,3-linkage to the reducing GlcNAc as may be found in plants and invertebrates, e.g., insects and parasitic helminths. Starting with an established procedure for mass spectrometric peptide mapping, the anal. of N-glycans by matrix-assisted laser desorption/ionization mass spectrometry involved the use of peptide:N-glycosidase A, a triphasic microcolumn for sample cleanup, and a new matrix mixture consisting of 2,5-dihydroxybenzoic acid, 1-hydroxyisoquinoline, and arabinosazone. The method was tested on proteins with N-glycans of known structure, i.e., as horseradish peroxidase, zucchini ascorbate oxidase, soybean agglutinin, honeybee venom hyaluronidase, bovine RNase B, and bovine fetuin. An electrophoretic band corresponding to 4 <SYM109>g of glycoprotein was generally sufficient to allow detection of the major N-glycan species. As an addnl. benefit, a peptide mass map is generated which serves to identify the analyzed protein. The method was applied to glycoprotein allergens whose glycan structures were unknown. Ara h 1 and Ole e 1, major allergens from peanut and olive pollen, resp., contained mainly xylosylated N-glycans with the composition Man3(-4)XylGlcNAc2 in the case of Ara h 1 and GlcNAc1-2Man3XylGlcNAc2 in the case of Ole e 1 where also some GlcNAc0-2Man3XylFucGlcNAc2 was found. (c) 2000 Academic Press. REFERENCE COUNT: 56

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DOCUMENT NUMBER: 132:120806
TITLE: "Modified expression of plasma glutathione peroxidase and manganese superoxide dismutase in human renal cell carcinoma"
AUTHOR(S): *Sarto, Cecilia; Frutiger, Severine; Cappellano, Francesco; Sanchez, Jean-Charles; Doro, Giancarlo; Catanzaro, Francesco; Hughes, Graham J.; Hochstrasser, Denis F.; Mocarelli, Paolo*
CORPORATE SOURCE: University Department of Clinical Pathology, Desio Hospital, Desio-Milan, I-20033, Italy
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AB Two-dimensional polyacrylamide gel electrophoresis (2-D PAGE) is a powerful tool to sep. thousands of polypeptides and to highlight the modification of protein expression in malignant diseases. By applying 2-D PAGE to ten normal human kidney and ten homologous renal cell carcinoma (RCC) tissues, we found two peptides in all ten normal tissues but not in RCCs and, conversely, two peptides were detected in all RCCs but not in normal tissues. Using matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF-MS) and internal sequence anal., the two first peptides were identified as two isoforms of plasma glutathione peroxidase (GPxP). The two other peptides isolated in all RCCs but not in normal tissues were identified by N-terminal sequence anal. as multimeric forms of manganese superoxide dismutase (Mn-SOD). No multimeric Mn-SODs and only two monomeric forms were detected in normal tissues. GPxP and Mn-SOD are metallo-enzymes encoded on chromosome 5q32 and on chromosome 6p25, resp. Their regions are within the locus 5q21 <SYM174> qter and 6q21-6q27 on which deletions and translocations are described in some cytogenetic studies of RCC transformation. Therefore, our results might suggest a correlation between the modified expression of GPxP and Mn-SOD in tumor tissues and chromosomal modifications, and that the two proteins may be putative markers for diagnosis of RCC. REFERENCE COUNT: 55